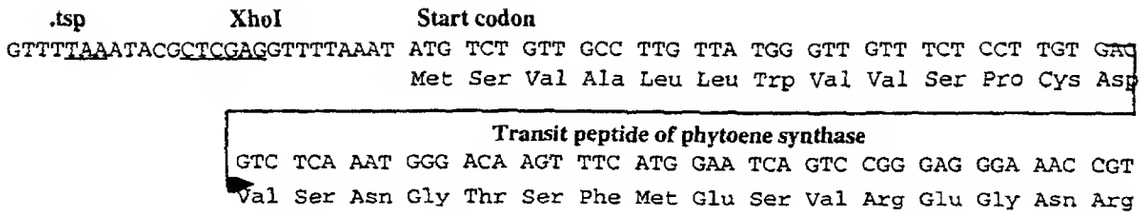

.tsp
XhoI
Start codon
GTTTTAAATACGCTCGAGGTTTTAAAT ATG TCT GTT GCC TTG TTA TGG GTT GTT TCT CCT TGT GAC
Met Ser Val Ala Leu Leu Trp Val Val Ser Pro Cys Asp
Transit peptide of phytoene synthase
GTC TCA AAT GGG ACA AGT TTC ATG GAA TCA GTC CGG GAG GGA AAC CGT
Val Ser Asn Gly Thr Ser Phe Met Glu Ser Val Arg Glu Gly Asn Arg

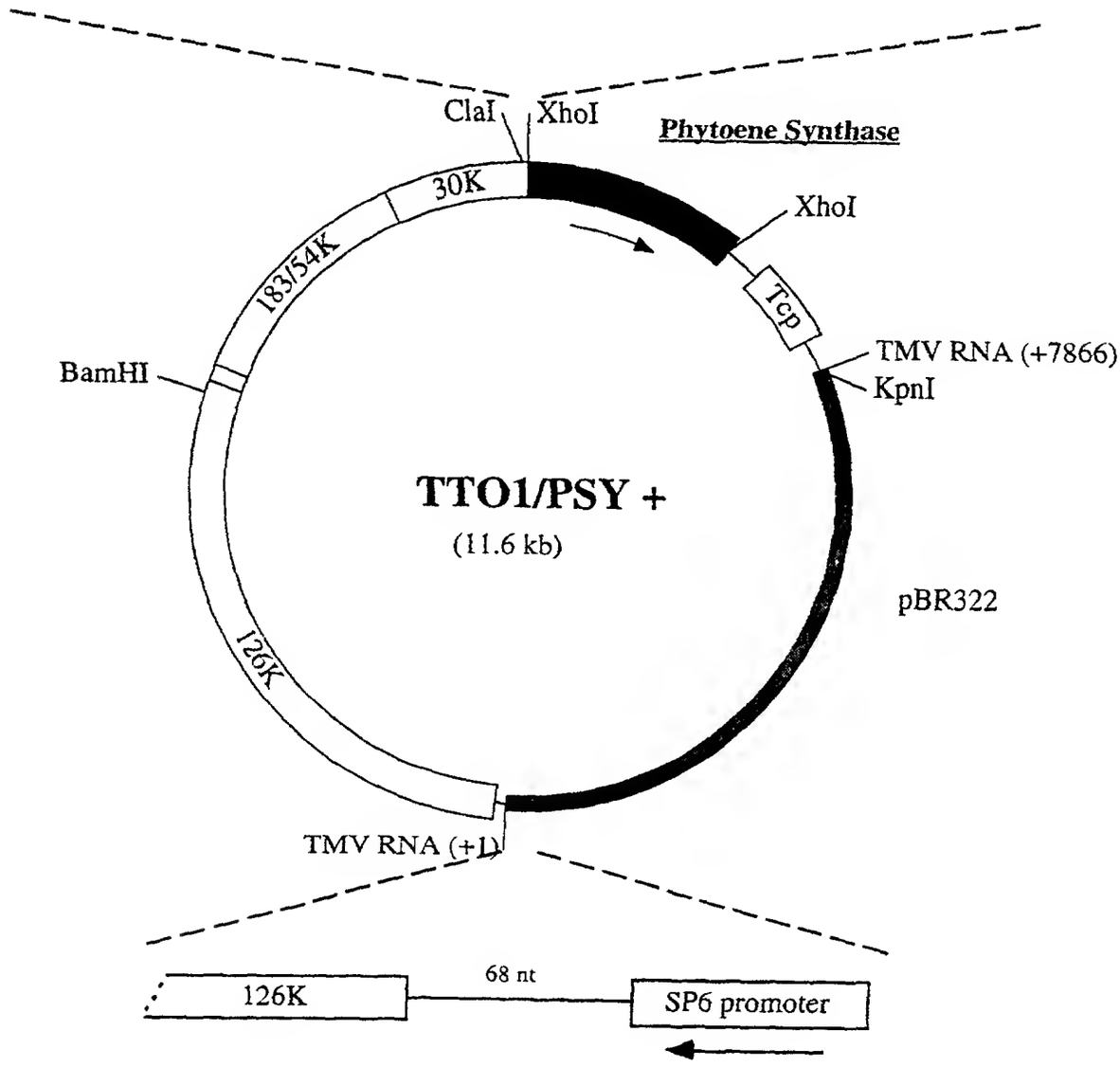

ClaI
XhoI
Phytoene Synthase
30K
XhoI
183/54K
Tcp
TMV RNA (+7866)
BamHI
KpnI
TTO1/PSY +
(11.6 kb)
pBR322
126K
TMV RNA (+1)
68 nt
126K
SP6 promoter

Figure 1

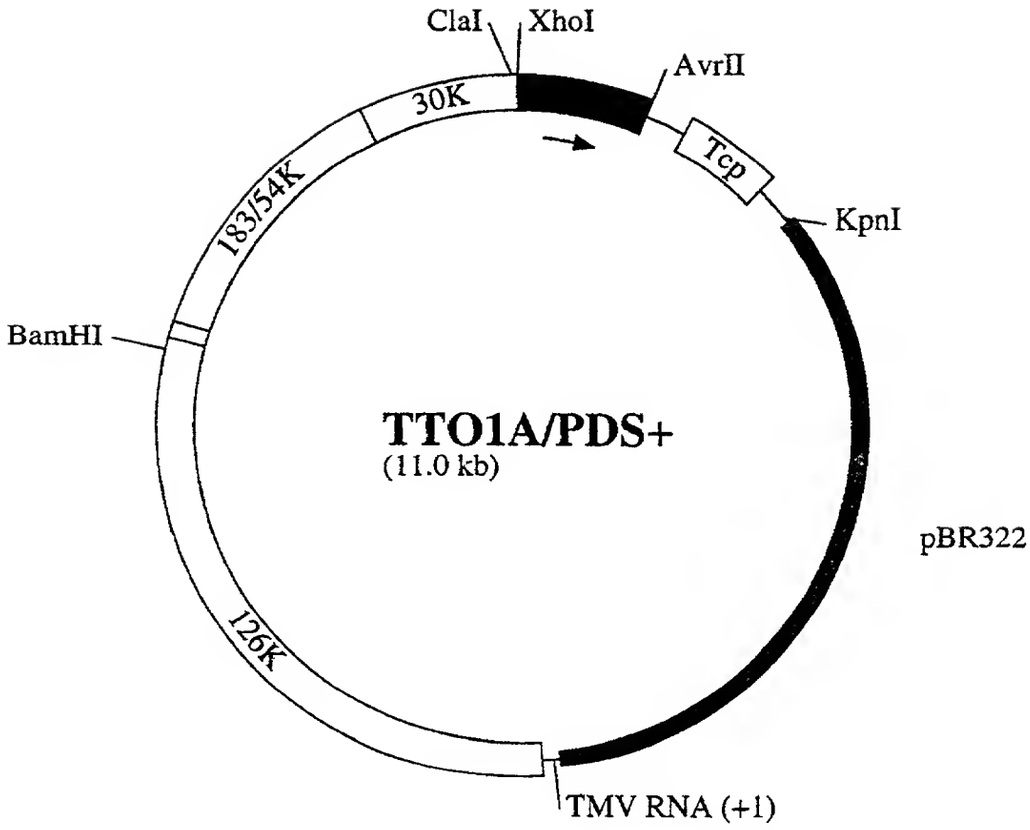
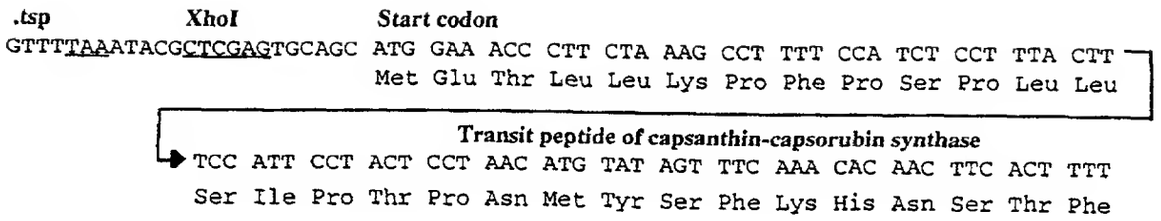

ClaI
XhoI
AvrII
30K
Tcp
KpnI
183/54K
BamHI
TTO1A/PDS+
(11.0 kb)
pBR322
126K
TMV RNA (+1)

Figure 2


.tsp
XhoI
Start codon
GTTTTAAATACGCTCGAGTGCAGC ATG GAA ACC CTT CTA AAG CCT TTT CCA TCT CCT TTA CTT
Met Glu Thr Leu Leu Lys Pro Phe Pro Ser Pro Leu Leu
Transit peptide of capsanthin-capsorubin synthase
TCC ATT CCT ACT CCT AAC ATG TAT AGT TTC AAA CAC AAC TTC ACT TTT
Ser Ile Pro Thr Pro Asn Met Tyr Ser Phe Lys His Asn Ser Thr Phe

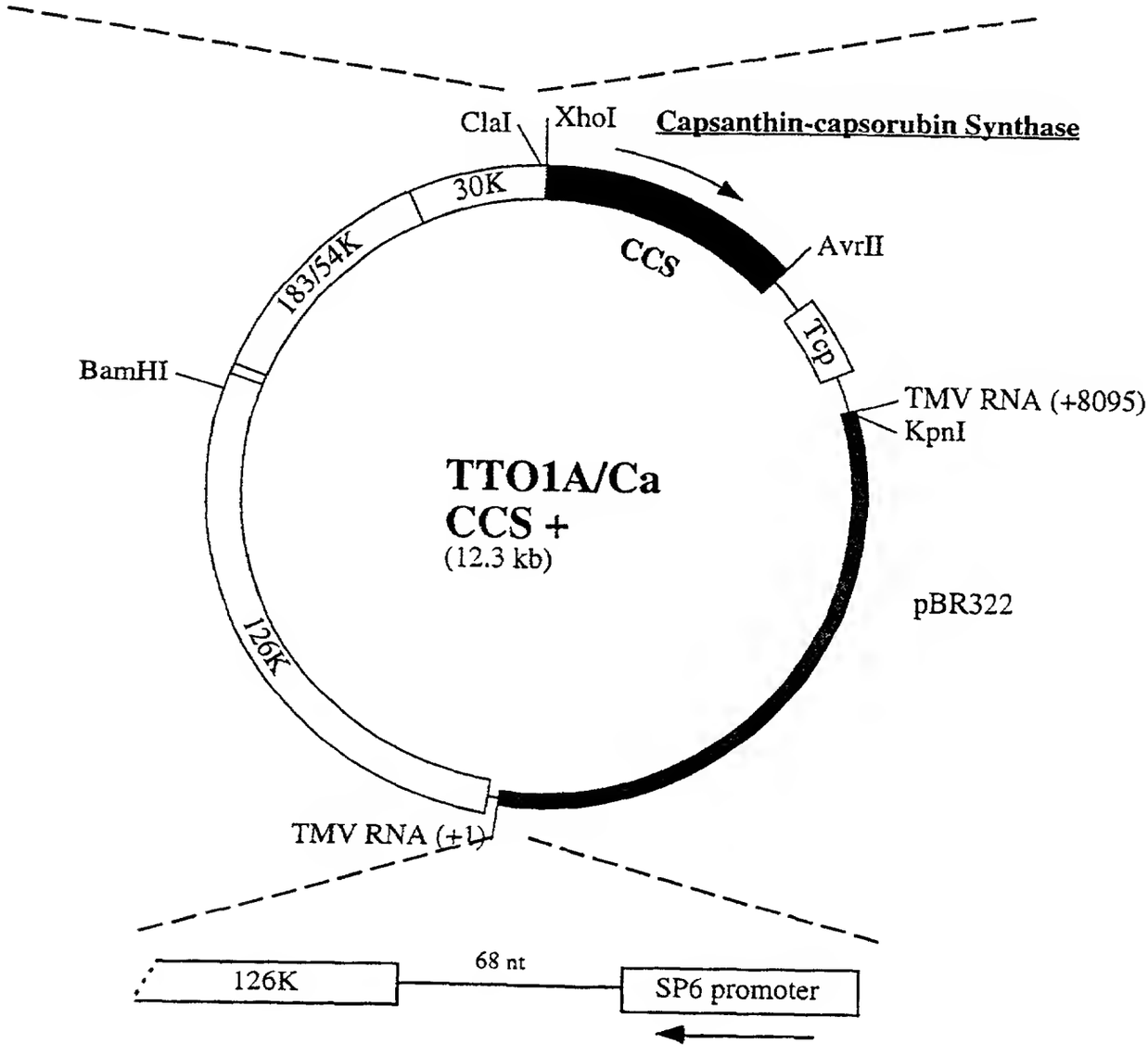

ClaI
XhoI
Capsanthin-capsorubin Synthase
30K
183/54K
CCS
AvrII
Tcp
BamHI
TMV RNA (+8095)
KpnI
TTO1A/Ca
CCS +
(12.3 kb)
pBR322
126K
TMV RNA (+1)
68 nt
126K
SP6 promoter

Figure 3

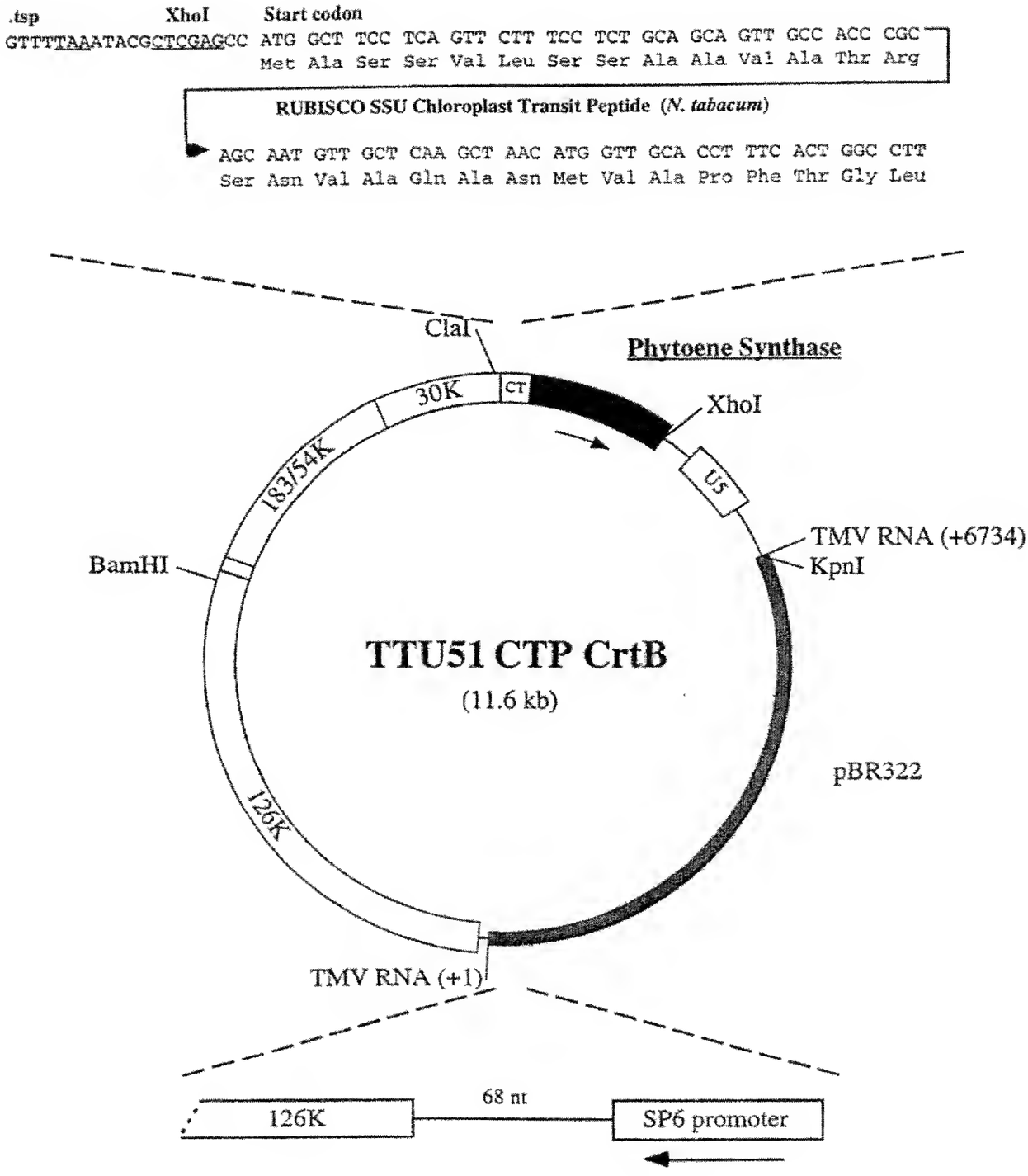

.tsp
XhoI
Start codon
GTTTTAAATACGCTCGAGCC ATG GCT TCC TCA GTT CTT TCC TCT GCA GCA GTT GCC ACC CGC
Met Ala Ser Ser Val Leu Ser Ser Ala Ala Val Ala Thr Arg
RUBISCO SSU Chloroplast Transit Peptide (N. tabacum)
AGC AAT GTT GCT CAA GCT AAC ATG GTT GCA CCT TTC ACT GGC CTT
Ser Asn Val Ala Gln Ala Asn Met Val Ala Pro Phe Thr Gly Leu
ClaI
Phytoene Synthase
30K
CT
XhoI
U5
183/54K
TMV RNA (+6734)
KpnI
BamHI
TTU51 CTP CrtB
(11.6 kb)
pBR322
126K
TMV RNA (+1)
68 nt
126K
SP6 promoter

Figure 4

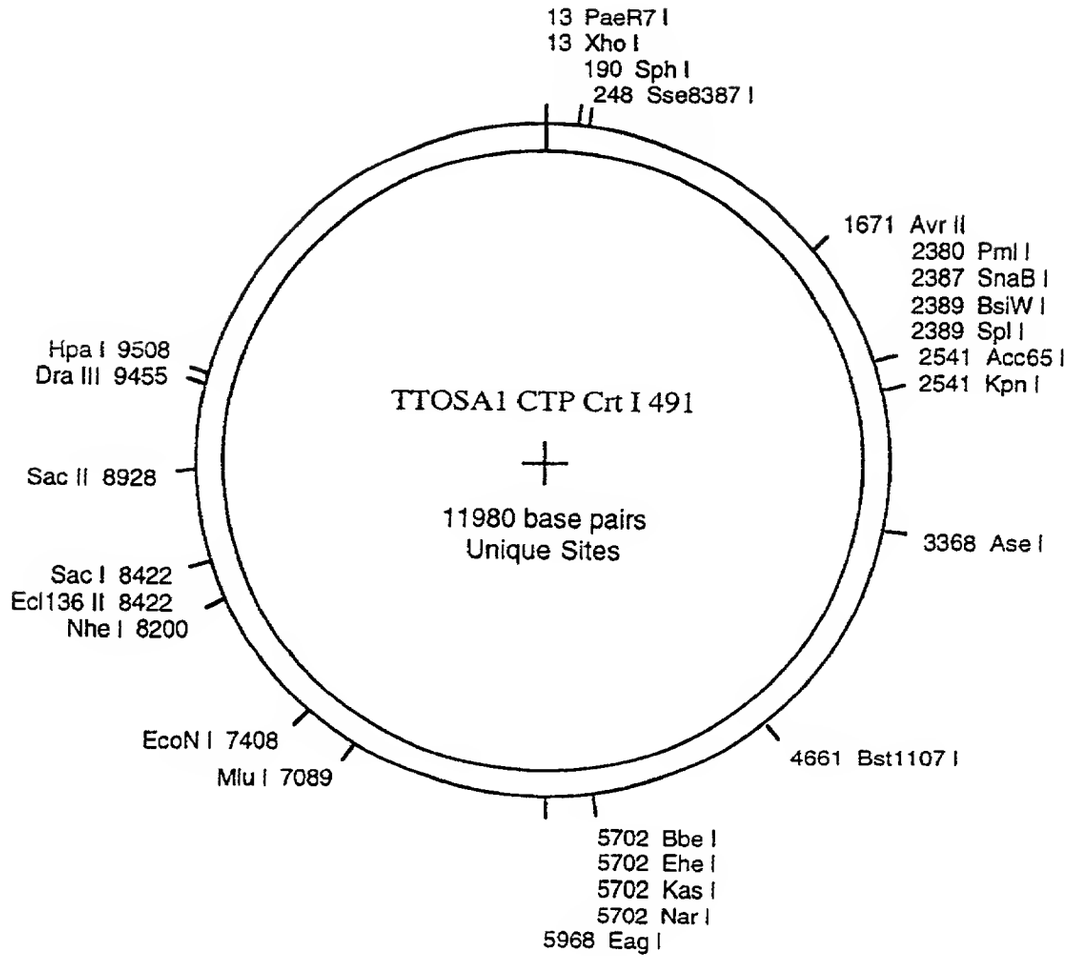

13 PaeR7 I
13 Xho I
190 Sph I
248 Sse8387 I
1671 Avr II
2380 Pml I
2387 SnaB I
2389 BsiW I
2389 Spl I
2541 Acc65 I
2541 Kpn I
3368 Ase I
4661 Bst1107 I
5702 Bbe I
5702 Ehe I
5702 Kas I
5702 Nar I
5968 Eag I
EcoN I 7408
Mlu I 7089
Sac I 8422
Ecl136 II 8422
Nhe I 8200
Sac II 8928
Hpa I 9508
Dra III 9455
TTOSA1 CTP Crt I 491
11980 base pairs
Unique Sites

Figure 5

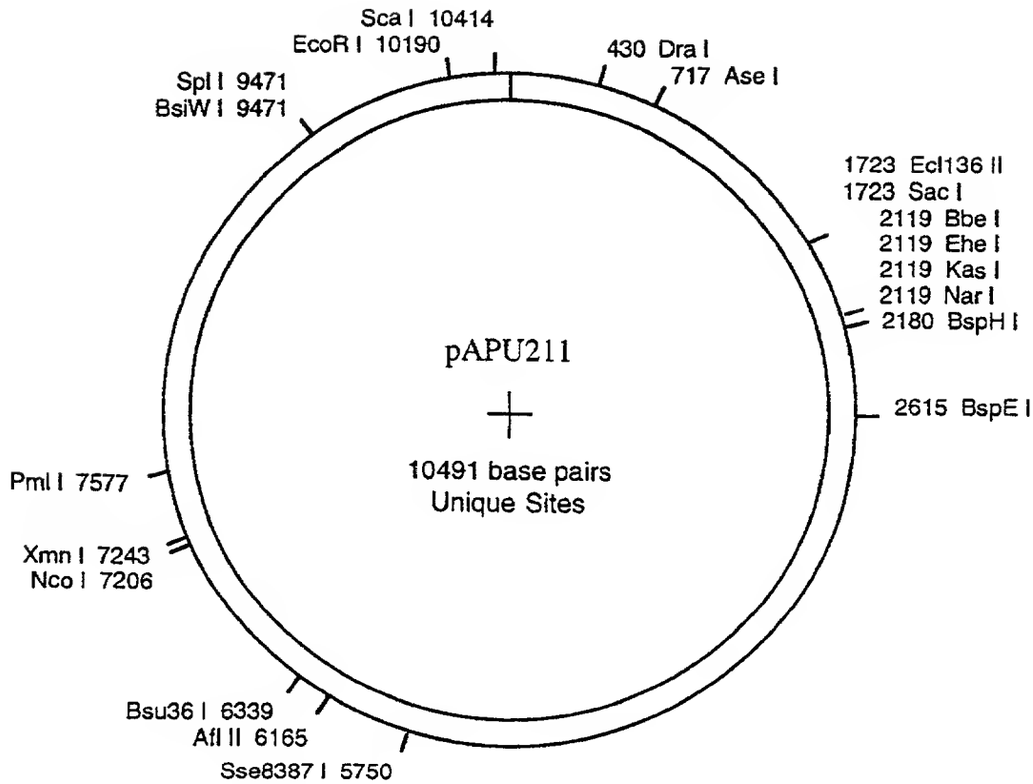

Sca I 10414
EcoR I 10190
430 Dra I
717 Ase I
Spl I 9471
BsiW I 9471
1723 Ecl136 II
1723 Sac I
2119 Bbe I
2119 Ehe I
2119 Kas I
2119 Nar I
2180 BspH I
pAPU211
2615 BspE I
10491 base pairs
Unique Sites
Pml I 7577
Xmn I 7243
Nco I 7206
Bsu36 I 6339
Afl II 6165
Sse8387 I 5750

Figure 6

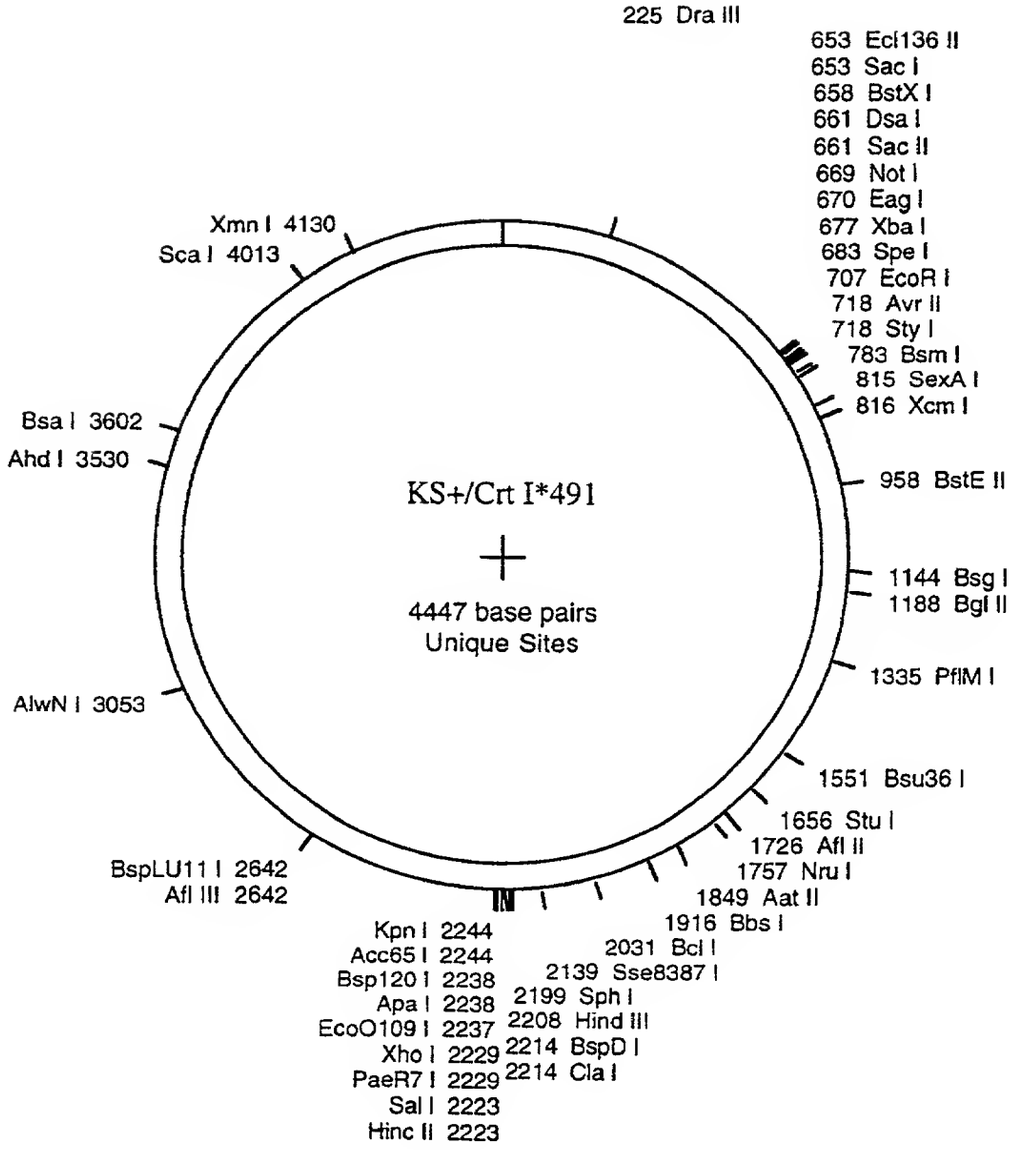

225 Dra III
653 Ecl136 II
653 Sac I
658 BstX I
661 Dsa I
661 Sac II
669 Not I
670 Eag I
677 Xba I
683 Spe I
707 EcoR I
718 Avr II
718 Sty I
783 Bsm I
815 SexA I
816 Xcm I
958 BstE II
1144 Bsg I
1188 Bgl II
1335 PflM I
1551 Bsu36 I
1656 Stu I
1726 Afl II
1757 Nru I
1849 Aat II
1916 Bbs I
2031 Bcl I
2139 Sse8387 I
2199 Sph I
2208 Hind III
2214 BspD I
2214 Cla I
Kpn I 2244
Acc65 I 2244
Bsp120 I 2238
Apa I 2238
EcoO109 I 2237
Xho I 2229
PaeR7 I 2229
Sal I 2223
Hinc II 2223
BspLU11 I 2642
Afl III 2642
AlwN I 3053
Ahd I 3530
Bsa I 3602
Xmn I 4130
Sca I 4013
KS+/Crt I*491
4447 base pairs
Unique Sites

Figure 7

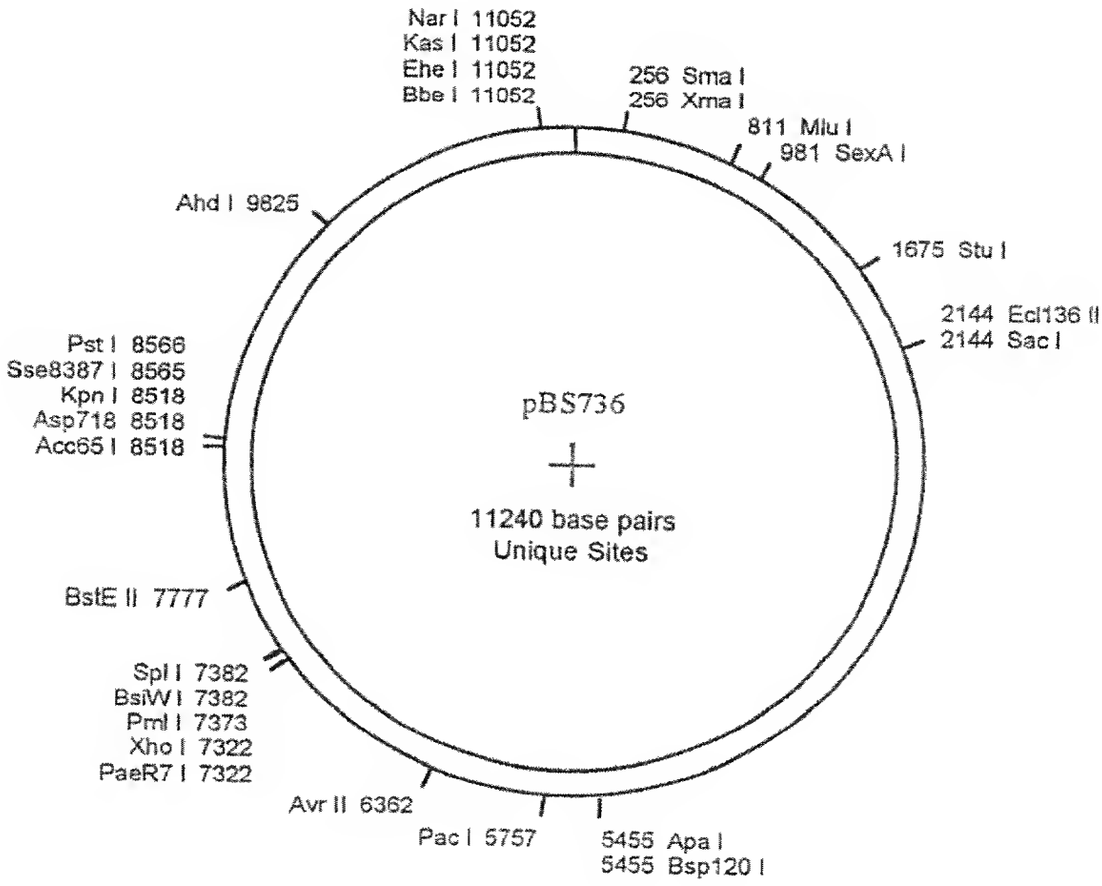

Nar I 11052
Kas I 11052
Ehe I 11052
Bbe I 11052
256 Sma I
256 Xma I
811 Mlu I
981 SexA I
1675 Stu I
2144 Ecl136 II
2144 Sac I
5455 Apa I
5455 Bsp120 I
Pac I 5757
Avr II 6362
PaeR7 I 7322
Xho I 7322
Pml I 7373
BsiW I 7382
Spl I 7382
BstE II 7777
Acc65 I 8518
Asp718 8518
Kpn I 8518
Sse8387 I 8565
Pst I 8566
Ahd I 9825
pBS736
11240 base pairs
Unique Sites

Figure 8

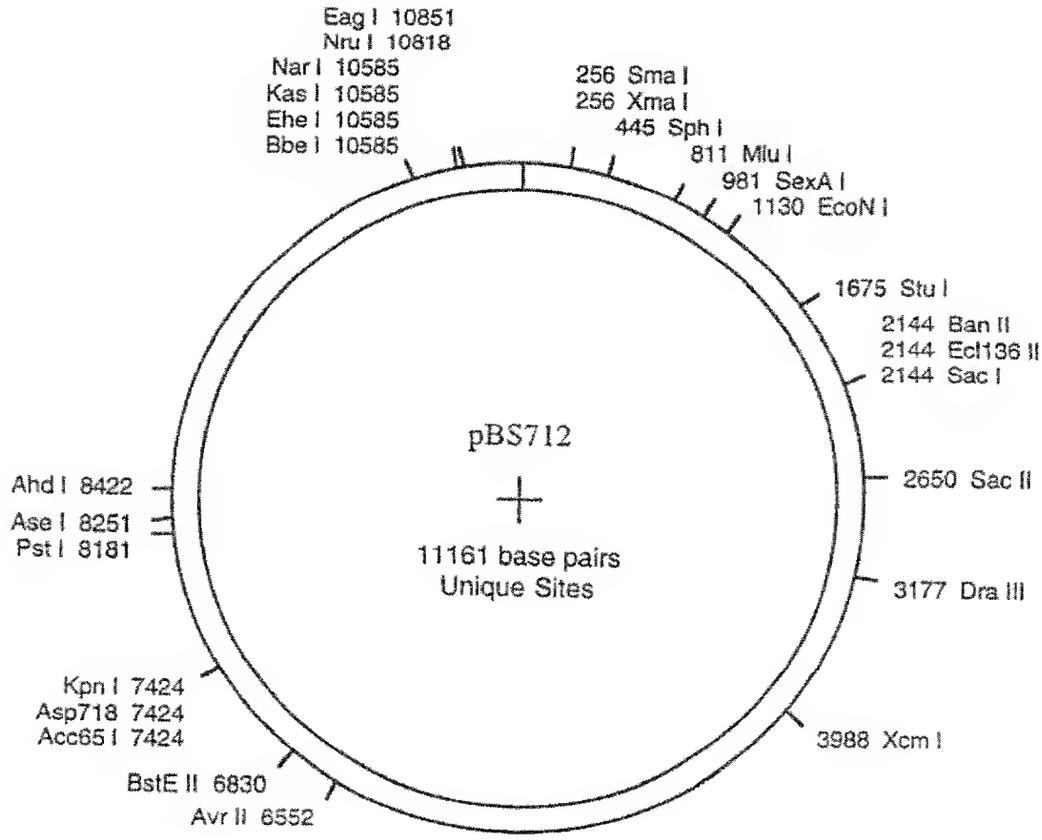

Eag I 10851
Nru I 10818
Nar I 10585
Kas I 10585
Ehe I 10585
Bbe I 10585
256 Sma I
256 Xma I
445 Sph I
811 Mlu I
981 SexA I
1130 EcoN I
1675 Stu I
2144 Ban II
2144 Ecl136 II
2144 Sac I
2650 Sac II
3177 Dra III
3988 Xcm I
Kpn I 7424
Asp718 7424
Acc65 I 7424
BstE II 6830
Avr II 6552
Ahd I 8422
Ase I 8251
Pst I 8181
pBS712
11161 base pairs
Unique Sites

Figure 9

```
ATGGCTATTCCCGAAGAATTTGATATTATCGTCTGTGGTGGTGGATCCAGTGGATCCTGTATTGCCGGAAGATTGGCTAACTTGGATCAC   90
METAlaIleProGluGluPheAspIleIleValCysGlyGlyGlySerSerGlySerCysIleAlaGlyArgLeuAlaAsnLeuAspHis

TCCTTGAAAGTTGGTCTTATCGAAGCAGGTGAGAACAACCTCAACAACCCATGGGTTTACCTTCCAGGTATTTACCCAAGAAACATGAAG  180
SerLeuLysValGlyLeuIleGluAlaGlyGluAsnAsnLeuAsnAsnProTrpValTyrLeuProGlyIleTyrProArgAsnMETLys

TTGGACTCCAAGACTGCCTCTTTCTACACTGCCAACCCTTCTCCTCACTTGAACGGTAGAAGGGCTATTGTCCCATGTGCTAACATCTTG  270
LeuAspSerLysThrAlaSerPheTyrThrAlaAsnProSerProHisLeuAsnGlyArgArgAlaIleValProCysAlaAsnIleLeu

GGTGGTGGTTCTTCTATCAACTTCATGATGTACACCAGAGGTTCTGCTTCTGATTATGACGACTTAGAGGCTGAAGGATGGAAAACCAAG  360
GlyGlyGlySerSerIleAsnPheMETMETTyrThrArgGlySerAlaSerAspTyrAspAspLeuGluAlaGluGlyTrpLysThrLys

GACTTGCTTCCATTGATGAAAAAGACCGAGACCTACCAAAGAGCTTGCAACAACCCTGATATCCACGGTTTTGAGGGTCCAATCAAGGTT  450
AspLeuLeuProLeuMETLysLysThrGluThrTyrGlnArgAlaCysAsnAsnProAspIleHisGlyPheGluGlyProIleLysVal

TCTTTCGGTAACTACACCTACCCAGTCTGTCAAGATTTCTTGAGAGCAAGTGAATCCCAAGGTATTCCTTACGTTGATGACTTGGAAGAC  540
SerPheGlyAsnTyrThrTyrProValCysGlnAspPheLeuArgAlaSerGluSerGlnGlyIleProTyrValAspAspLeuGluAsp

TTGGTTACCGCTCATGGTGCTGAGCACTGGTTGAAGTGGATCAACAGAGACACTGGTCGTCGTTCCGACTCCGCCCACGCCTTTGTCCAC  630
LeuValThrAlaHisGlyAlaGluHisTrpLeuLysTrpIleAsnArgAspThrGlyArgArgSerAspSerAlaHisAlaPheValHis

TCTACCATGAGAAATCACGACAACTTGTACTTGATCTGCAACACCAAGGTTGAGAAGATCATTGTTGAAGACGGAAGAGCTGTCGGTGTT  720
SerThrMETArgAsnHisAspAsnLeuTyrLeuIleCysAsnThrLysValGluLysIleIleValGluAspGlyArgAlaValGlyVal

AAAACCGTTCCAAGCAAGCCTTTGAACCCAAAGAAGCCAAGTCACAAGATTTACCGTGCTAGAAAGCAGATCGTTTTGTCTTGTGGTACC  810
LysThrValProSerLysProLeuAsnProLysLysProSerHisLysIleTyrArgAlaArgLysGlnIleValLeuSerCysGlyThr

ATCTCTTCGCCTTTGGTCTTGCAAAGATCTGGTTTCGGTGACCCAGTTAAATTGAGAGCCGCTGGTGTTAAGCCTTTGGTTAACTTGCCA  900
IleSerSerProLeuValLeuGlnArgSerGlyPheGlyAspProValLysLeuArgAlaAlaGlyValLysProLeuValAsnLeuPro

GGTGTTGGTAGAAACTTCCAGGACCACTACTGTTTCTTCACTCCTTACAGAATCAAGCCTCAATACGAGTCCTTCGATGACTTTGTCCGT  990
GlyValGlyArgAsnPheGlnAspHisTyrCysPhePheThrProTyrArgIleLysProGlnTyrGluSerPheAspAspPheValArg

GGTGACGCTGAGATTCAAAAGAGAGTCTTTGACCAATGGTACGCCAATGGTACTGGTCCTTTGGCCACCAACGGTATTGAAGCCGGTGTC 1080
GlyAspAlaGluIleGlnLysArgValPheAspGlnTrpTyrAlaAsnGlyThrGlyProLeuAlaThrAsnGlyIleGluAlaGlyVal

AAGATCAGACCAACTCCTGAGGAAATGGCTCAAATGGACGAATCCTTCCAAGAAGGTTACAGAGAATACTTTGAAGACAAGCCAGACAAG 1170
LysIleArgProThrProGluGluMETAlaGlnMETAspGluSerPheGlnGluGlyTyrArgGluTyrPheGluAspLysProAspLys

CCAGTTATGCACTACTCTATCATTGCTGGTTTCTTCGGTGACCACACCAAGATTCCTCCTGGAAAGTACATGACCATGTTCCACTTCTTG 1260
ProValMETHisTyrSerIleIleAlaGlyPhePheGlyAspHisThrLysIleProProGlyLysTyrMETThrMETPheHisPheLeu

GAGTACCCATTCTCTAGAGGTTCTATCCACATTACCTCACCAGACCCATATGCAACTCCAGACTTTGACCCAGGTTTCATGAACGATGAA 1350
GluTyrProPheSerArgGlySerIleHisIleThrSerProAspProTyrAlaThrProAspPheAspProGlyPheMETAsnAspGlu

AGAGACATGGCTCCTATGGTTTGGTCTTACAAGAAGTCTAGAGAGACTGCCAGAAGAATGGACCACTTTGCCGGTGAAGTTACTTCTCAC 1440
ArgAspMETAlaProMETValTrpSerTyrLysLysSerArgGluThrAlaArgArgMETAspHisPheAlaGlyGluValThrSerHis

CACCCTCTGTTCCCATACTCATCTGAAGCCAGAGCTTACGAGATGGATTTGGAGACTTCCAACGCTTACGGTGGACCATTGAACTTGTCC 1530
HisProLeuPheProTyrSerSerGluAlaArgAlaTyrGluMETAspLeuGluThrSerAsnAlaTyrGlyGlyProLeuAsnLeuSer

GCTGGTCTTGCACACGGTTCTTGGACTCAACCTTTGAAGAAGCCAACTGCCAAGAACGAAGGTCACGTTACCTCCAACCAGGTTGAACTT 1620
AlaGlyLeuAlaHisGlySerTrpThrGlnProLeuLysLysProThrAlaLysAsnGluGlyHisValThrSerAsnGlnValGluLeu

CACCCAGACATCGAGTACGATGAGGAGGATGACAAGGCCATTGAGAACTACATCCGTGAGCACACTGAGACCACATGGCACTGTCTGGGA 1710
HisProAspIleGluTyrAspGluGluAspAspLysAlaIleGluAsnTyrIleArgGluHisThrGluThrThrTrpHisCysLeuGly

ACCTGTTCCATCGGTCCAAGAGAAGGTTCCAAGATTGTTAAATGGGGTGGTGTTCTAGACAACAGATCCAACGTTTACGGAGTCAAGGGC 1800
ThrCysSerIleGlyProArgGluGlySerLysIleValLysTrpGlyGlyValLeuAspAsnArgSerAsnValTyrGlyValLysGly

TTGAAGGTTGGTGACTTGTCTGTTTGTCCAGACAATGTTGGTTGTAACACTTACACTACCGCTCTTTTGATTGGTGAAAAGACTGCCACT 1890
LeuLysValGlyAspLeuSerValCysProAspAsnValGlyCysAsnThrTyrThrThrAlaLeuLeuIleGlyGluLysThrAlaThr

CTGGTTGGTGAAGACTTAGGATACTCTGGTGAGGCCTTAGACATGACTGTTCCACAATTCAAGTTGGGTACTTATGAGAAGACAGGTCTT 1980
LeuValGlyGluAspLeuGlyTyrSerGlyGluAlaLeuAspMETThrValProGlnPheLysLeuGlyThrTyrGluLysThrGlyLeu

GCTAGATTCTAA                                                                                    1992
AlaArgPheSTP
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Figure 10

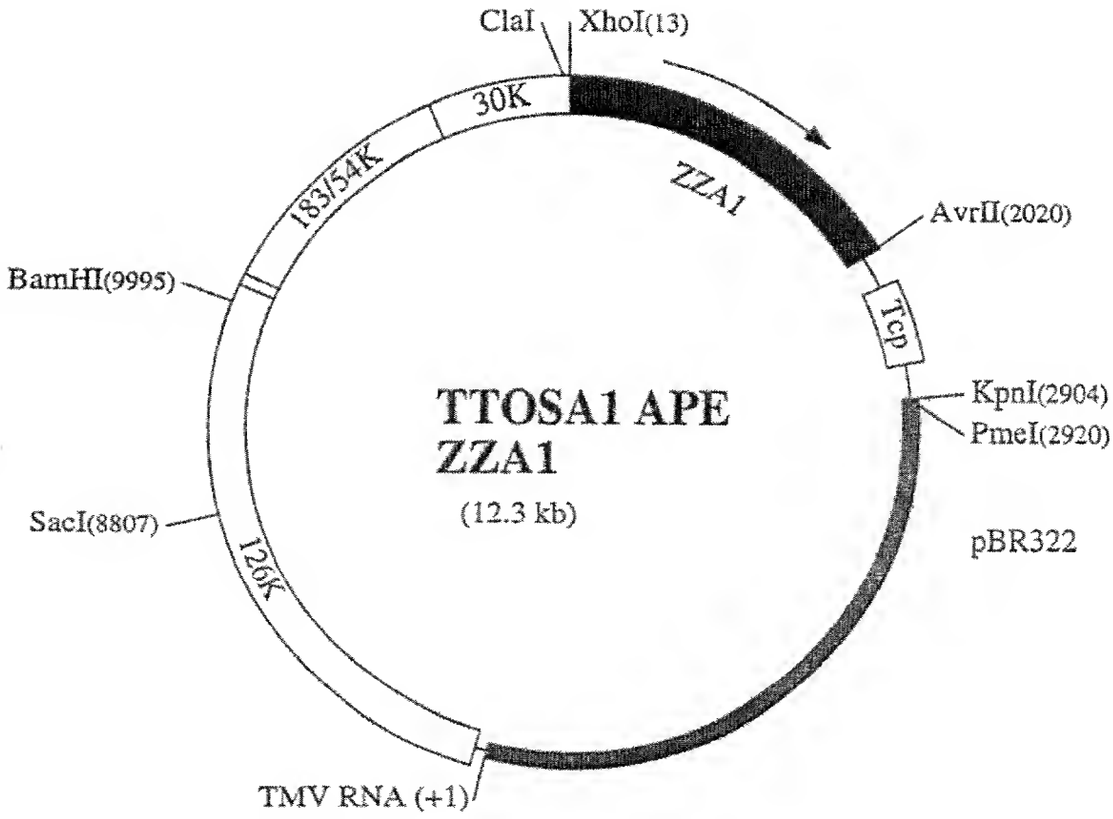
ClaI
XhoI(13)
30K
183/54K
ZZA1
AvrII(2020)
BamHI(9995)
Tcp
KpnI(2904)
PmeI(2920)
TTOSA1 APE
ZZA1
(12.3 kb)
pBR322
SacI(8807)
126K
TMV RNA (+1)

Figure 11

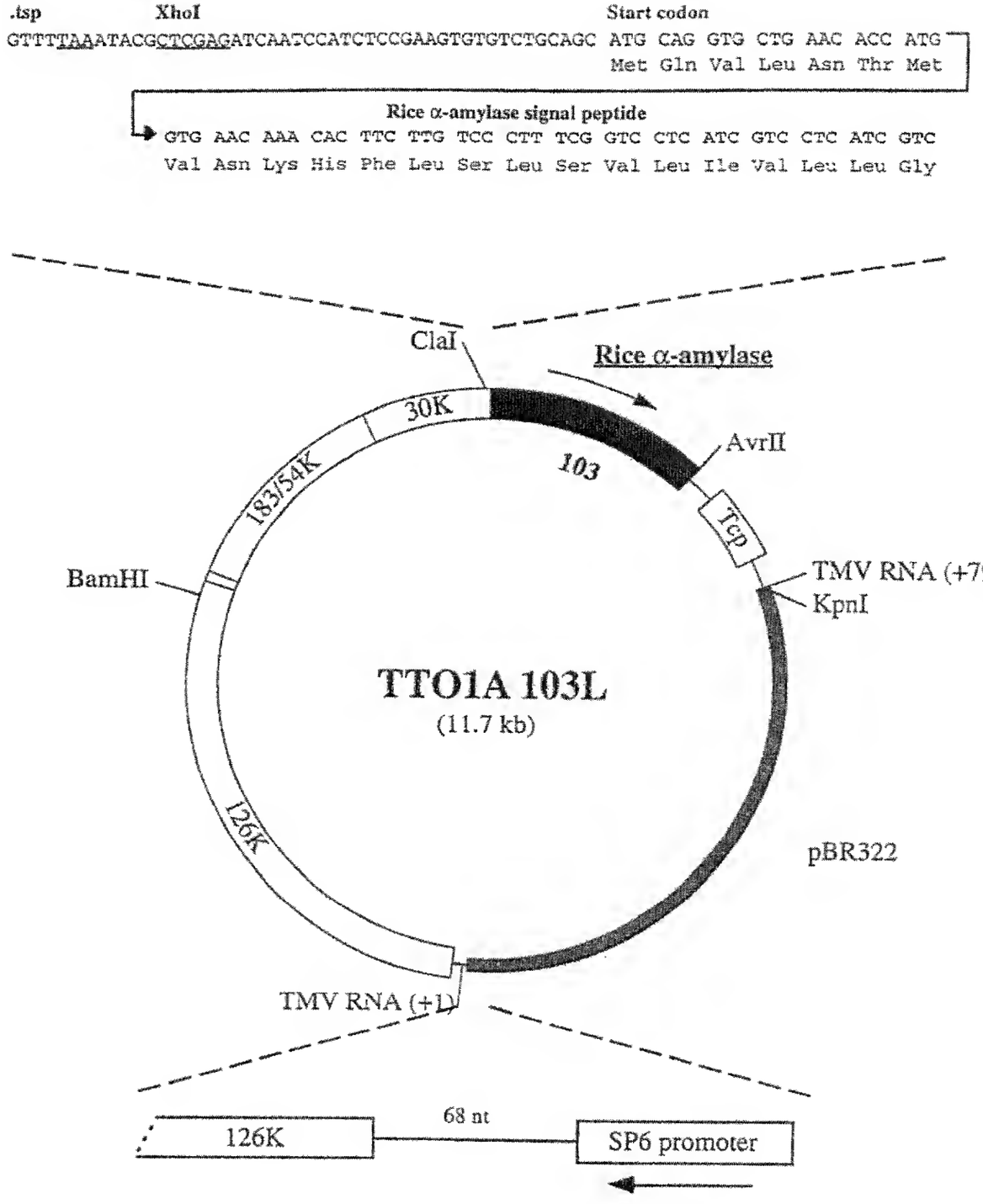
.tsp
XhoI
Start codon
GTTTTAAATACGCTCGAGATCAATCCATCTCCGAAGTGTGTCTGCAGC ATG CAG GTG CTG AAC ACC ATG
Met Gln Val Leu Asn Thr Met
Rice α-amylase signal peptide
GTG AAC AAA CAC TTC TTG TCC CTT TCG GTC CTC ATC GTC CTC ATC GTC
Val Asn Lys His Phe Leu Ser Leu Ser Val Leu Ile Val Leu Leu Gly
ClaI
Rice α-amylase
30K
183/54K
103
AvrII
Tcp
TMV RNA (+7930)
KpnI
BamHI
TTO1A 103L
(11.7 kb)
126K
pBR322
TMV RNA (+1)
68 nt
126K
SP6 promoter

Figure 12

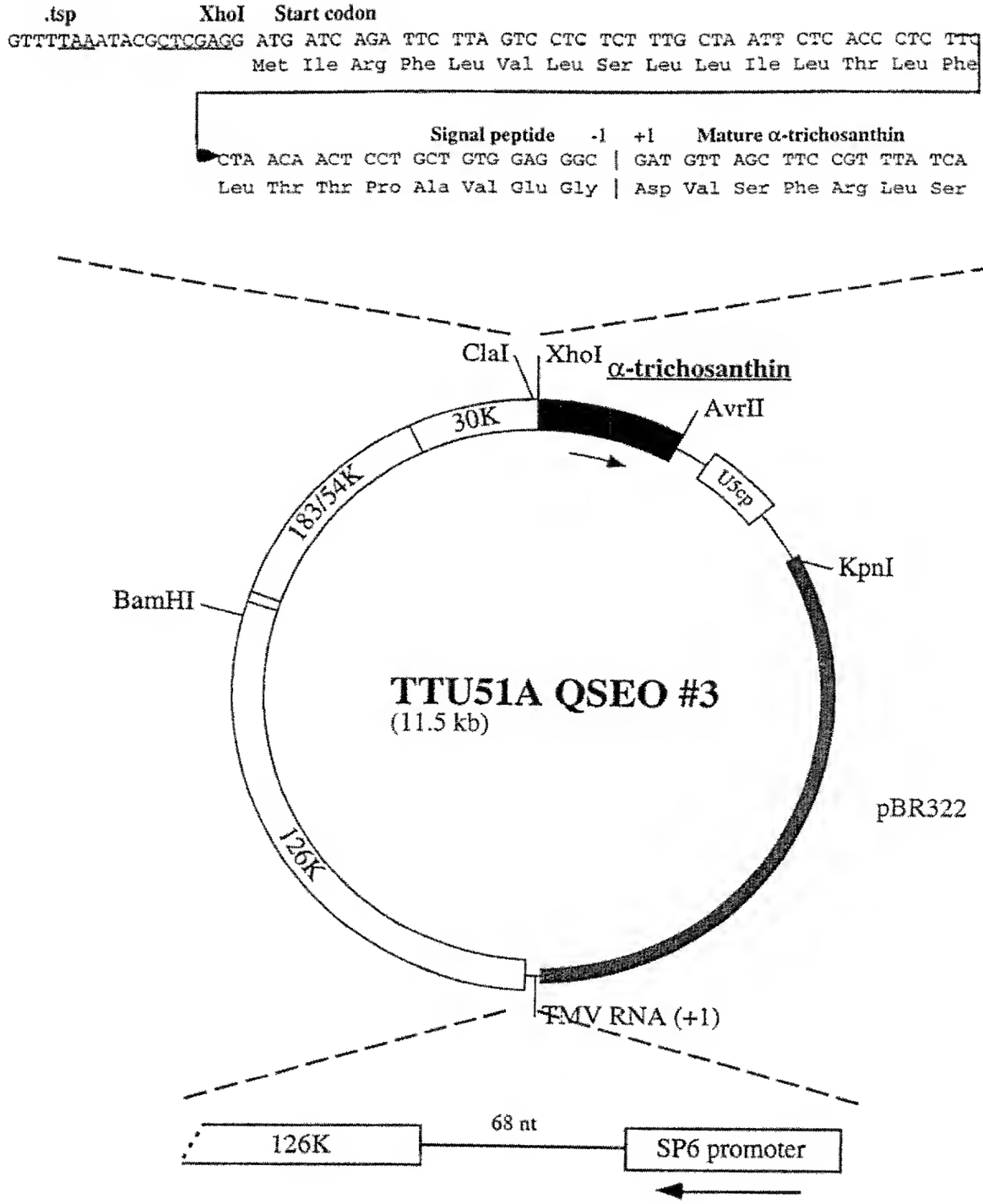
.tsp
XhoI
Start codon
GTTTTAAATACGCTCGAGG ATG ATC AGA TTC TTA GTC CTC TCT TTG CTA ATT CTC ACC CTC TTC
Met Ile Arg Phe Leu Val Leu Ser Leu Leu Ile Leu Thr Leu Phe
Signal peptide
-1
+1
Mature α-trichosanthin
CTA ACA ACT CCT GCT GTG GAG GGC | GAT GTT AGC TTC CGT TTA TCA
Leu Thr Thr Pro Ala Val Glu Gly | Asp Val Ser Phe Arg Leu Ser
ClaI
XhoI
α-trichosanthin
AvrII
30K
183/54K
U5cp
KpnI
BamHI
TTU51A QSEO #3
(11.5 kb)
pBR322
126K
TMV RNA (+1)
68 nt
126K
SP6 promoter

Figure 13

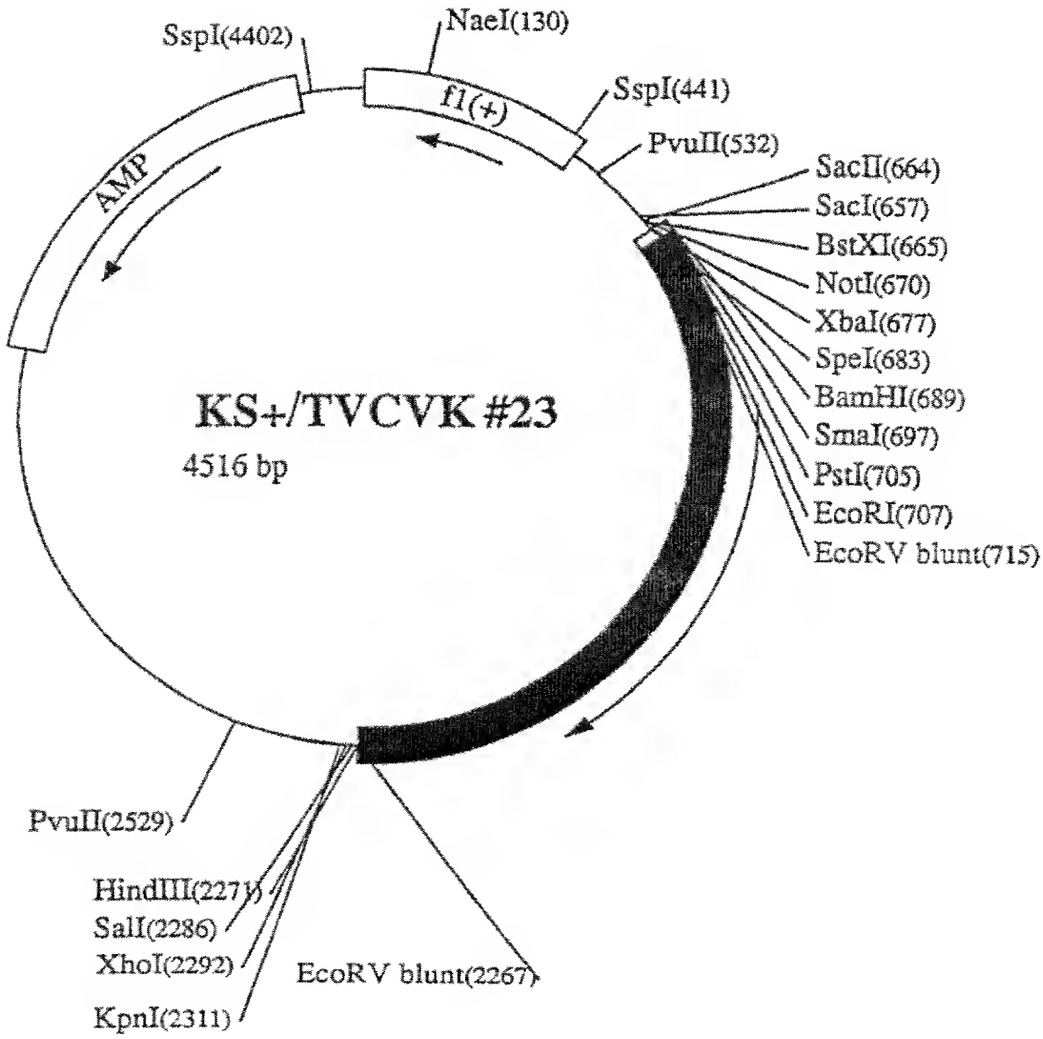
SspI(4402)
NaeI(130)
SspI(441)
f1(+)
PvuII(532)
AMP
SacII(664)
SacI(657)
BstXI(665)
NotI(670)
XbaI(677)
SpeI(683)
BamHI(689)
SmaI(697)
PstI(705)
EcoRI(707)
EcoRV blunt(715)
KS+/TVCVK #23
4516 bp
PvuII(2529)
HindIII(2271)
SalI(2286)
XhoI(2292)
KpnI(2311)
EcoRV blunt(2267)

Figure 14

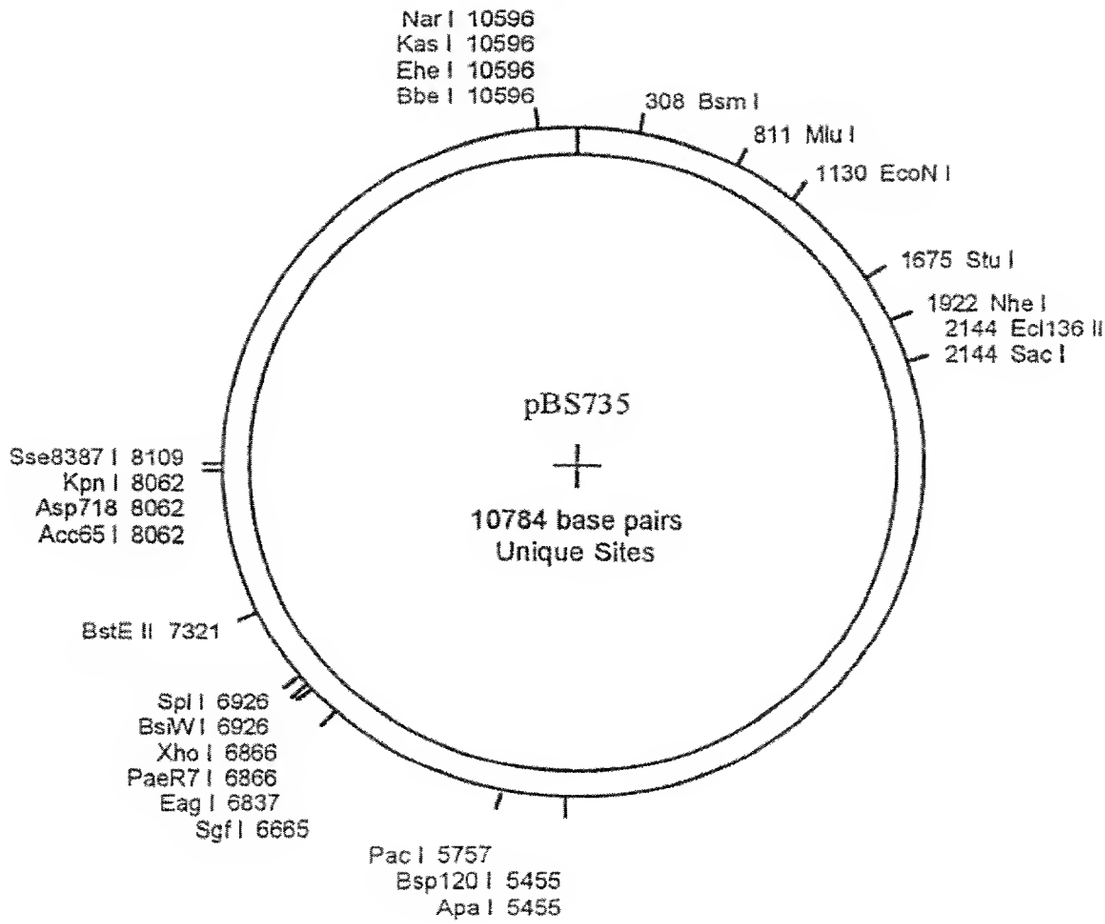
Nar I 10596
Kas I 10596
Ehe I 10596
Bbe I 10596
308 Bsm I
811 Mlu I
1130 EcoN I
1675 Stu I
1922 Nhe I
2144 Ecl136 II
2144 Sac I
pBS735
10784 base pairs
Unique Sites
Sse8387 I 8109
Kpn I 8062
Asp718 8062
Acc65 I 8062
BstE II 7321
Spl I 6926
BsiW I 6926
Xho I 6866
PaeR7 I 6866
Eag I 6837
Sgf I 6665
Pac I 5757
Bsp120 I 5455
Apa I 5455

Figure 15

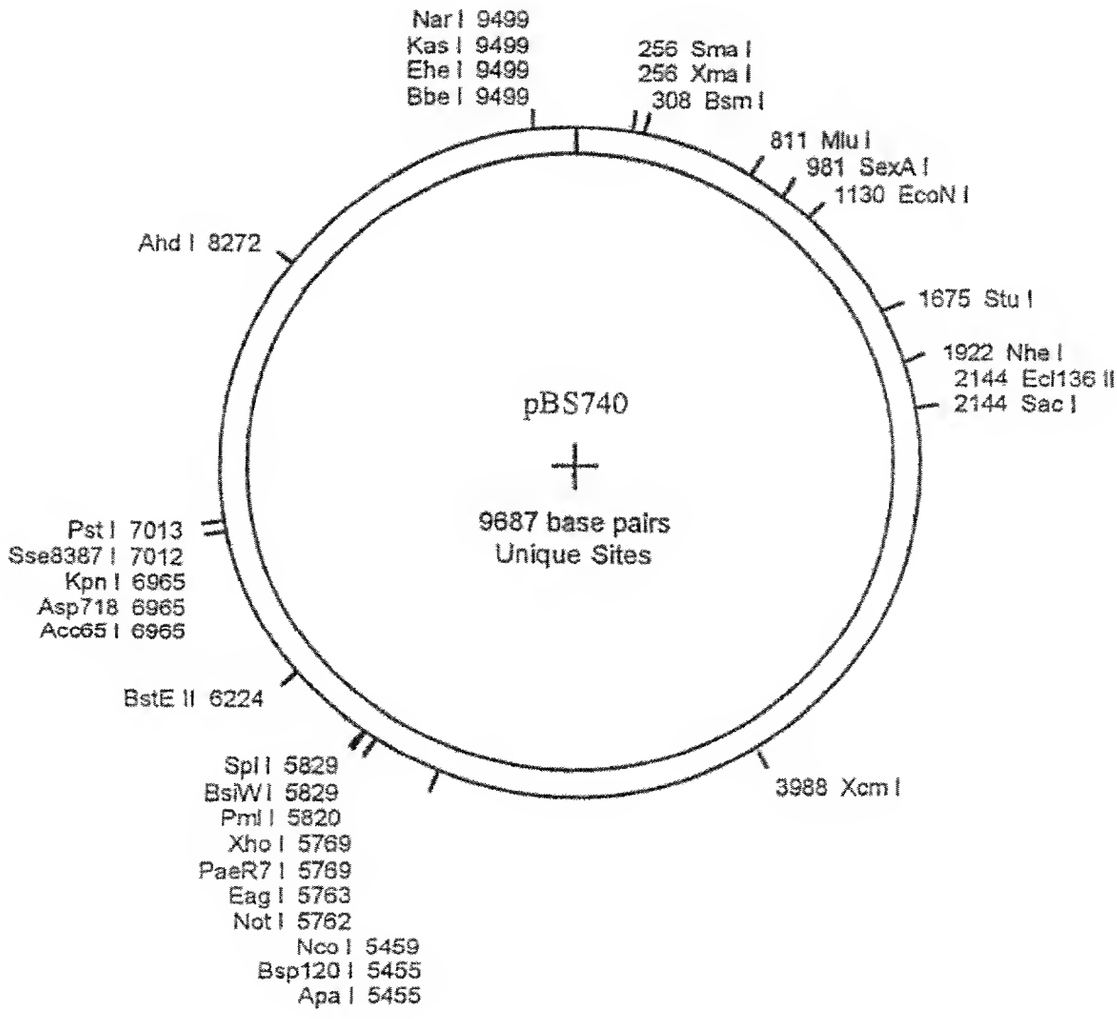
Nar I 9499
Kas I 9499
Ehe I 9499
Bbe I 9499
256 Sma I
256 Xma I
308 Bsm I
811 Mlu I
981 SexA I
1130 EcoN I
1675 Stu I
1922 Nhe I
2144 Ecl136 II
2144 Sac I
3988 Xcm I
Spl I 5829
BsiW I 5829
Pml I 5820
Xho I 5769
PaeR7 I 5769
Eag I 5763
Not I 5762
Nco I 5459
Bsp120 I 5455
Apa I 5455
BstE II 6224
Pst I 7013
Sse8387 I 7012
Kpn I 6965
Asp718 6965
Acc65 I 6965
Ahd I 8272
pBS740
9687 base pairs
Unique Sites

Figure 16

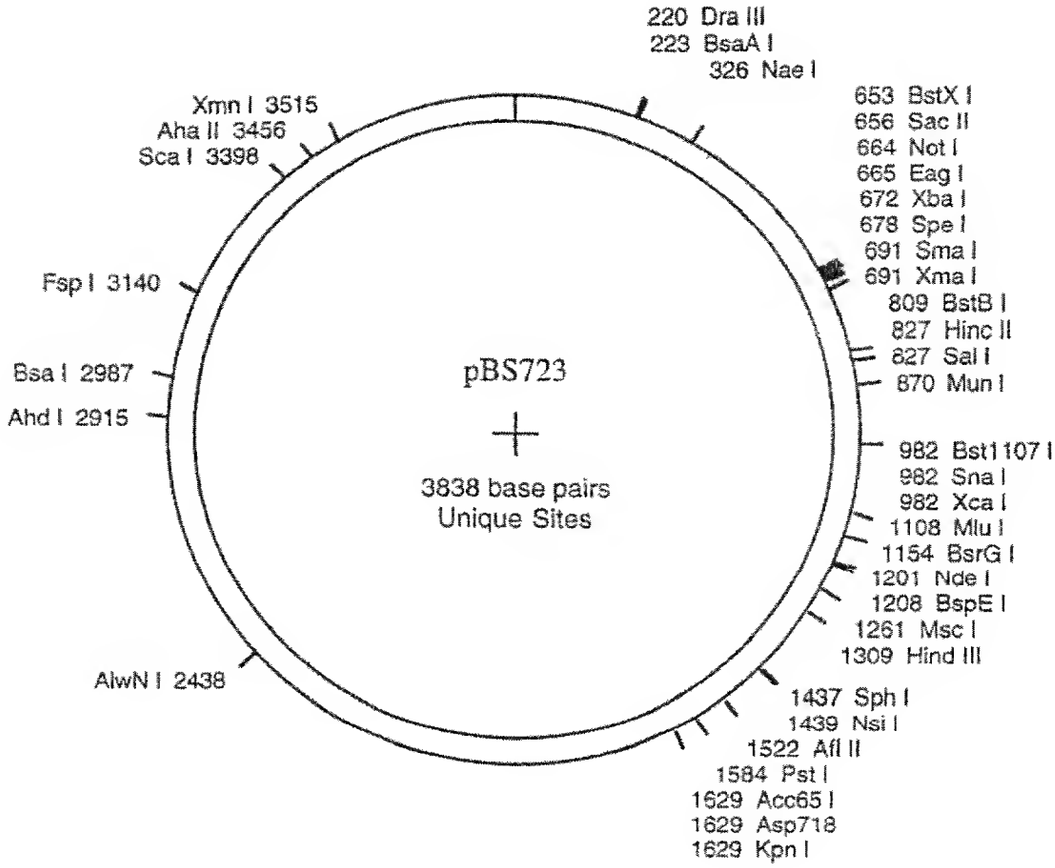
220 Dra III
223 BsaA I
326 Nae I
653 BstX I
656 Sac II
664 Not I
665 Eag I
672 Xba I
678 Spe I
691 Sma I
691 Xma I
809 BstB I
827 Hinc II
827 Sal I
870 Mun I
982 Bst1107 I
982 Sna I
982 Xca I
1108 Mlu I
1154 BsrG I
1201 Nde I
1208 BspE I
1261 Msc I
1309 Hind III
1437 Sph I
1439 Nsi I
1522 Afl II
1584 Pst I
1629 Acc65 I
1629 Asp718
1629 Kpn I
AlwN I 2438
Ahd I 2915
Bsa I 2987
Fsp I 3140
Sca I 3398
Aha II 3456
Xmn I 3515
pBS723
3838 base pairs
Unique Sites

Figure 17

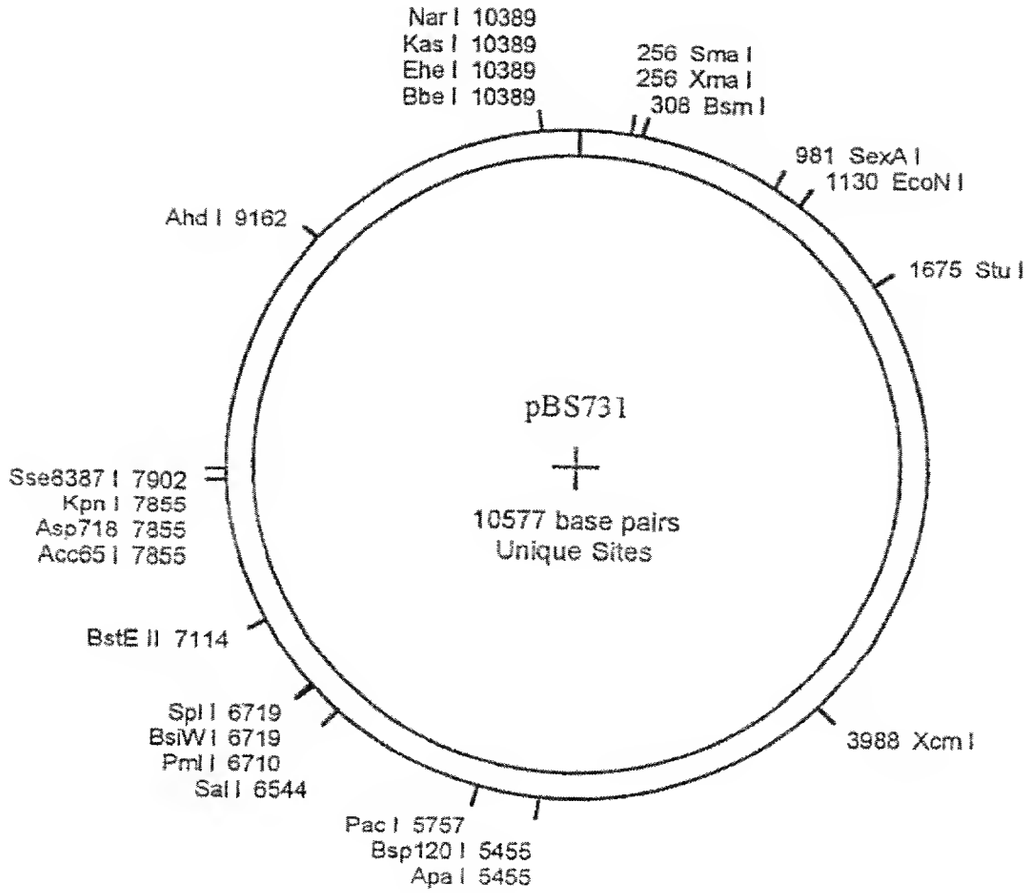
Nar I 10389
Kas I 10389
Ehe I 10389
Bbe I 10389
256 Sma I
256 Xma I
308 Bsm I
981 SexA I
1130 EcoN I
1675 Stu I
3988 Xcm I
Pac I 5757
Bsp120 I 5455
Apa I 5455
Spl I 6719
BsiW I 6719
Pml I 6710
Sal I 6544
BstE II 7114
Sse8387 I 7902
Kpn I 7855
Asp718 7855
Acc65 I 7855
Ahd I 9162
pBS731
10577 base pairs
Unique Sites

Figure 18

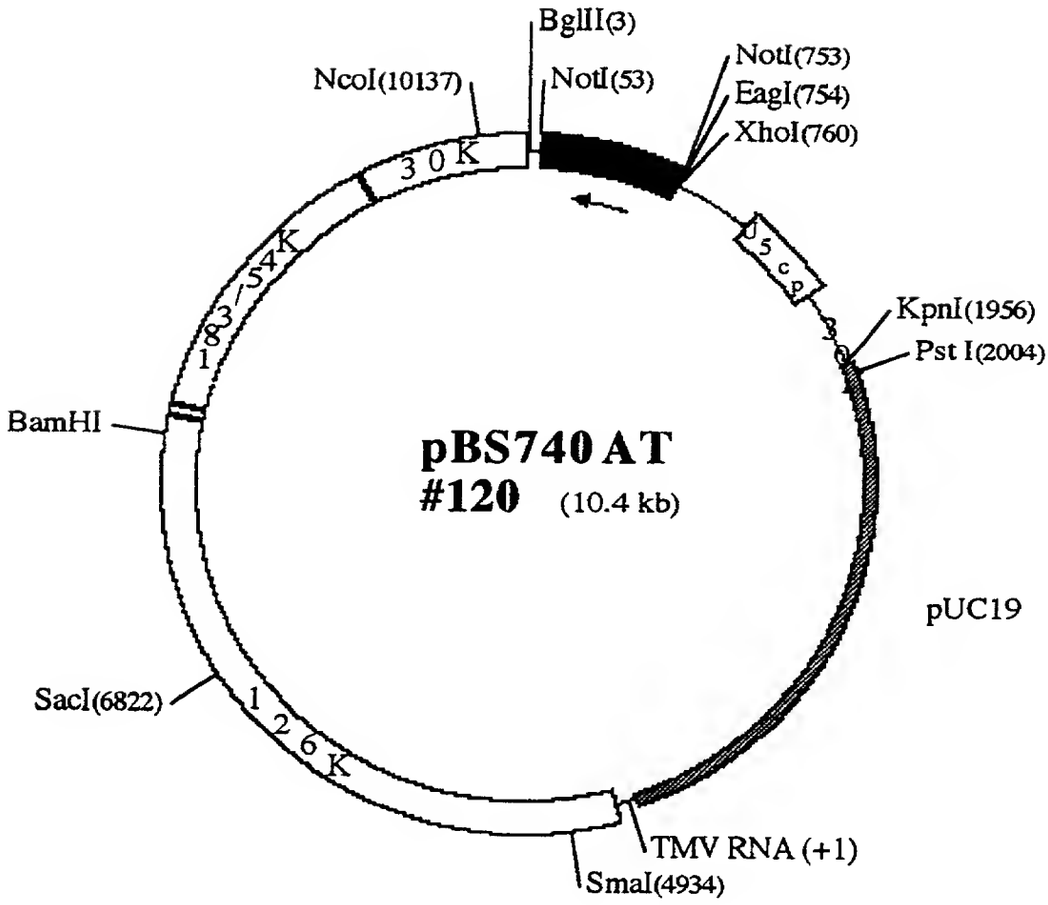
BglII(3)
NcoI(10137)
NotI(53)
NotI(753)
EagI(754)
XhoI(760)
30K
U5
cp
KpnI(1956)
Pst I(2004)
3
54K
38/1
BamHI
pBS740 AT
#120 (10.4 kb)
pUC19
SacI(6822)
126K
TMV RNA (+1)
SmaI(4934)

Figure 19

Nucleotide sequence alignment of 740 AT #120 to human ADP-ribosylation factor (ARF3) M33384

```
740 AT #120    AAGAAGGAGATGCGAATTCTGATGGTTGGTCTTGATGCTGCTGGTAAGACCACAATCTTG
               |||||||||||||||  ||  ||||||||  ||  ||  |||||  ||  ||  ||||||||  |||  |
M33384         AAGAAGGAGATGCGCATCCTGATGGTGGGCCTGGATGCCGCAGGAAAGACCACCATCCTA
               K  K  E  M  R  I  L  M  V  G  L  D  A  A  G  K  T  T  I  L

740 AT #120    TACAAGCTCAAGCTCGGAGAGATTGTCACCACCATCCCTACTATTGGTTTCAATGTGGAA
               ||||||||  ||  ||  ||  |||||  ||||||||||||||||||  |||||  ||||||||||||
M33384         TACAAGCTGAAACTGGGGGAGATCGTCACCACCATCCCTACCATTGGGTTCAATGTGGAG
               Y  K  L  K  L  G  E  I  V  T  T  I  P  T  I  G  F  N  V  E

740 AT #120    ACTGTGGAATACAAGAACATTAGTTTCACCGTGTGGGATGTCGGGGGTCAGGACAAGATC
               ||  |||||  ||  |||||||||  ||  ||  ||  ||||||||||||  ||  ||  ||||||||||||
M33384         ACAGTGGAGTATAAGAACATCAGCTTTACAGTGTGGGATGTGGGTGGCCAGGACAAGATT
               T  V  E  Y  K  N  I  S  F  T  V  W  D  V  G  G  Q  D  K  I

740 AT #120    CGTCCCTTGTG-AGACACTACTTCCAGAACACTCAAGGTCTAATCTTTGTTGTTGATAGC
               ||  |||  |  ||  ||||||||||||||||||||  |||||  |  ||  |||||  ||  ||  |||
M33384         CGACCCCTCTGGAGACACTACTTCCAGAACACCCAAGGGTTGATATTTGTGGTCGACAGC
               R  P  L  W  R  H  Y  F  Q  N  T  Q  G  L  I  F  V  V  D  S

740 AT #120    AATGACAGAGACAGAGTTGTTGAGGCTCGAGATGAACTCCACAGGATGCTGAATGAGGAC
               |||||  |  ||  ||||  ||||||  ||  ||  ||  ||  ||  ||||||  ||||||
M33384         AATGATCGGGAGCGAGTAAATGAGGCCCGGGAAGAGCTGATGAGAATGCTGGCGGAGGAC
               N  D  R  E  R  V  N  E  A  R  E  E  L  M  R  M  L  A  E  D

740 AT #120    GAGCTGCGTGATGCTGTGTTGCTTGTGTTTGCCAACAAGCAAGATCTTCCAAATGCTATG
               |||||  ||  ||||||||  |  |||||  |||||  |||||  ||  |||||  ||  ||||||||||
M33384         GAGCTCCGGGATGCTGTACTCCTTGTCTTTGCAAACAAACAGGATCTGCCTAATGCTATG
               E  L  R  D  A  V  L  L  V  F  A  N  K  Q  D  L  P  N  A  M

740 AT #120    AACGCTGCTGAAATCACAGATAAGCTTGGCCTTCACTCCCTCCGTCAGCGTCATTGGTAT
               ||||||||||||  ||||||||  |||||  |||||  ||  |||||  |||||  |||  |  |||||
M33384         AACGCTGCTGAGATCACAGACAAGCTGGGCCTGCATTCCCTTCGTCACCGTAACTGGTAC
               N  A  A  E  I  T  D  K  L  G  L  H  S  L  R  H  R  N  W  Y

740 AT #120    ATCCAGAGCACATGTGCCACTTCAGGTGAAGGGCTTTATGAAGGTCTGGACTGGCT
               ||  |||  |||  ||||||||  ||  ||  |||||  ||  |||||  ||||||||||||
M33384         ATTCAGGCCACCTGTGCCACCAGCGGGGACGGGCTGTACGAAGGCCTGGACTGGCT
               I  Q  A  T  C  A  T  S  G  D  G  L  Y  E  G  L  D  W  L
```

Figure 20

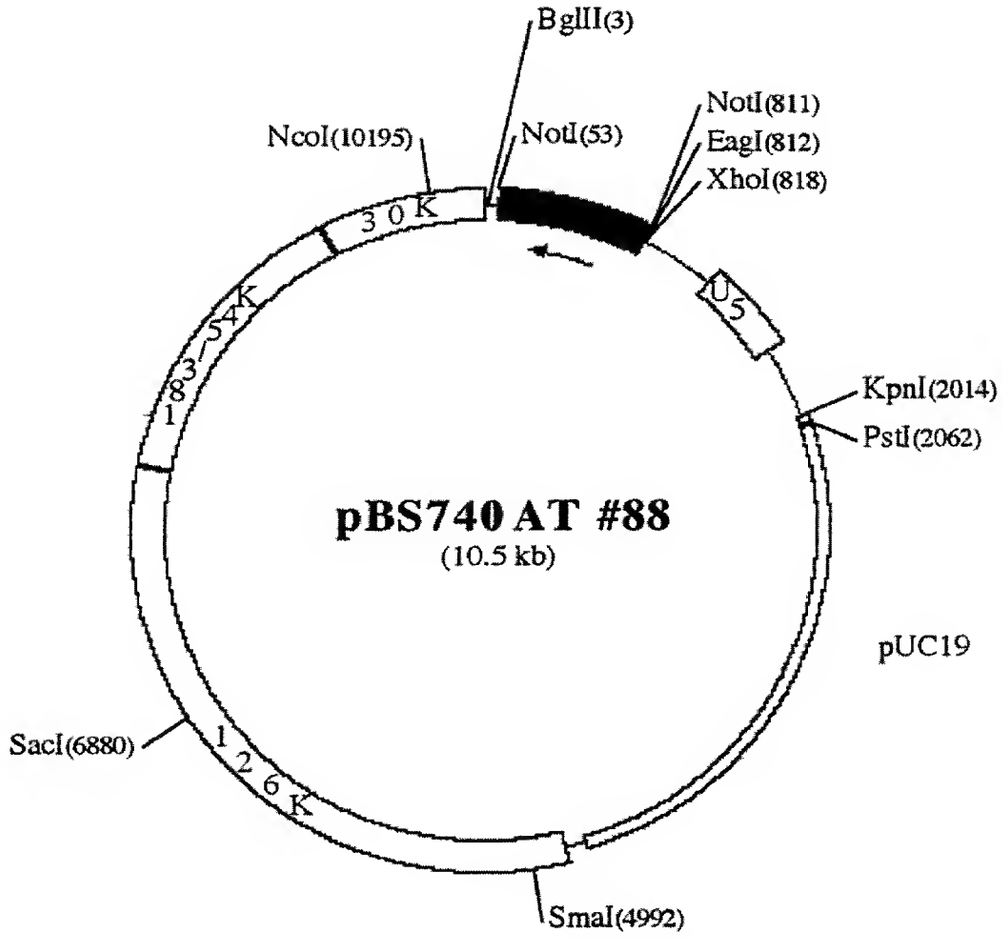
BglII(3)
NotI(811)
EagI(812)
XhoI(818)
NcoI(10195)
NotI(53)
30K
54K
38K
U5
KpnI(2014)
PstI(2062)
pBS740 AT #88
(10.5 kb)
pUC19
SacI(6880)
126K
SmaI(4992)

Figure 21

Nucleotide sequence alignment of 740 AT #88 to L33574 mRNA for rhodopsin

```
740 AT #88      CAACCTCCCGTTGGTGTTCCTCCTCCTCAAGGTTATCCACCGGAGGGATATCCAAAAGAT
                ||||||||||| ||||||||||||||||||||||||| ||||||| ||| ||||||||
L33574          CAACCTCCCGTCGGTGTTCCTCCTCCTCAAGGTTATCCCCCGGAGGATTATTCAAAAGAT

740 AT #88      GCTTATCCACCACAAGGATATCCTCCTCAGGGATATCCTCAGCAAG GCTATCCACCTCA
                ||||||||||| ||||||||||||||||||||||||| ||||||| ||| ||||||||
L33574          GCTTATCCACCGCAAGGATATCCTCCTCAGGGCTATCCGCCGCAAGTACCCTCCACAGCA

740 AT #88      GGGATATCCTCAACAAGGTTATCCTCAGCAAGGATATCC
                ||||||||| |  ||||| || ||||  ||||| |||||
L33574          GGGATATCCGCCGCAAGG TACCCTCCACAAGGCTATCC
```

Identities = 45/57 (78%), Positives = 45/57 (78%)

Figure 22

Nucleotide sequence alignment of 740 AT #88 to X07797
Octopus mRNA for rhodopsin

```
740 AT #88      CCACCACAAGGATATCCTCCTCAGGGATATCCTCAGCAAGGCTATCCACCTCAGGGA
                ||||||||||||  ||  ||  ||  ||  ||  ||  |  ||||||||  |||||  ||||||
X07797          CCACCACAAGGCTACCCACCACAAGGCTACCCACCTCAAGGCTACCCACCCCAGGGA
```

Identities = 45/57 (78%), Positives = 45/57 (78%)

Figure 23

G-protein-coupled receptor

N. benthamiana

```
740 AT #88      YPPQ-GYPPQGYPQQGYPPQGYPQQGYPQQGYPPPYAPQYPPPPQASATTEQVLA
                |||   |||| |||   |||| ||   |||| |||||||      |    |          ||
ATTS2938        YPPKDGYPPAGYPPAGYPPPGY-AQGYPEQGYPPPQYSQAPEEKQNAGMLEGCLA
```

Figure 24

G-protein-coupled receptor

N. benthamiana

```
740 AT #88          PPVGV-PPPQGYPPEGYPKDAYPPQGYPPQGYPQQGYPPQGYPQQGYPQQGY
                    ||  |   |||||||||+|||    ||||||||||| |  |    |||  |  ||   |  ||
octopus rhodopsin   PPQGAYPPPQGYPPQGYPPQGYPPQGYPPQGAPPQVEAPQGAPPQGVDNQAY
```

Identity = 34/54 65%, Posititives 35/52 66%

Figure 25

Amino acid sequence comparison of 740 AT #2441 to tobacco RAN-B1 GTP binding protein

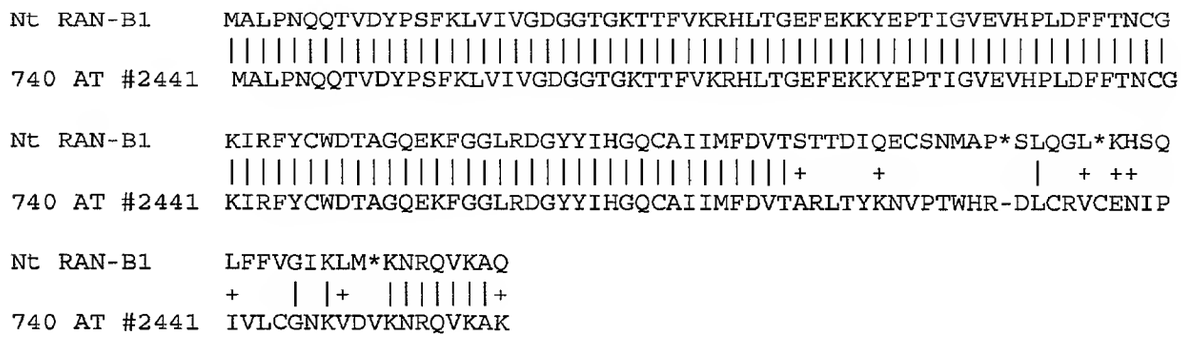

Figure 26

Nucleotide sequence comparison of 740 AT #2441 to human RAN GTP-binding protein

```
Human RAN       ACTGGAGAGTTTGAGAAGAAGTATGAACCCACTATTGGTGTTGAGGTTCATCC
                ||||| || ||||||||||||||||| | ||||  | ||||||||||||||||
740 AT #2241    ACTGGTGAATTTGAGAAGAAGTATGTAGCCACCTTGGGTGTTGAGGTTCATCC

Identities = 46/53 (86%), Positives = 46/53 (86%)
```

Figure 27

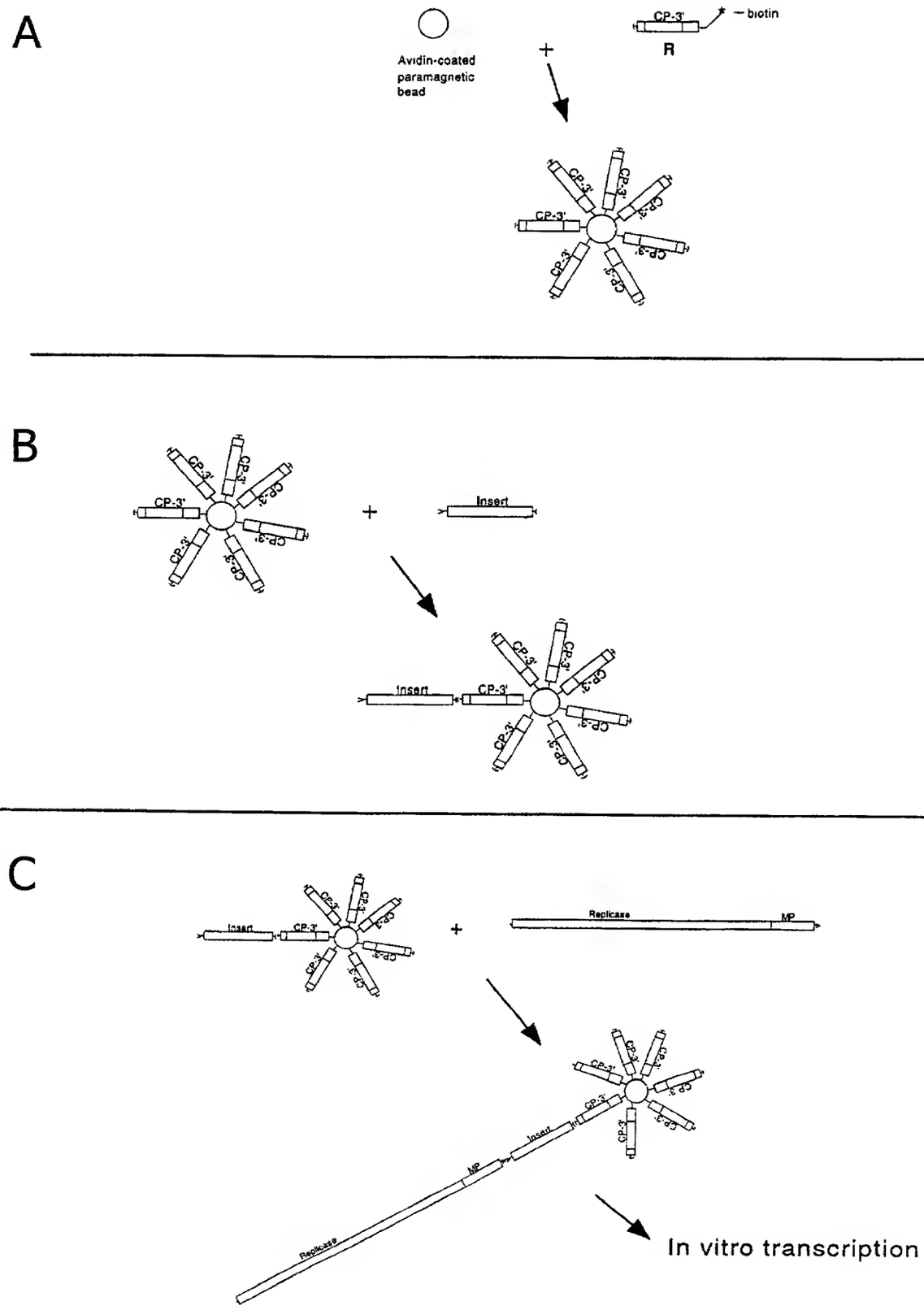
A
Avidin-coated
paramagnetic
bead
CP-3'
biotin
R
B
Insert
C
Replicase
MP
In vitro transcription

Figure 28